

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:29 ; Search time 170.72 Seconds
(without alignments)
27.443 Million cell updates/sec

Title: US-09-331-631A-3_COPY_117_185

Perfect score: 384

Sequence: 1 NR0RDPQOQYECOCERCORH.....EEQOREDEKEYEERMKEDD 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	175	45.6	566	2 S22477	vicilin precursor
2	149.5	38.9	588	1 FMCNAB	alpha-globulin B p
3	144	37.5	509	2 S08059	alpha-globulin typ
4	133	34.6	605	2 S06398	alpha-globulin typ
5	119.5	31.1	1038	2 T02634	rep protein homolo
6	117	30.5	810	2 T44430	protein pV100 (imp
7	113	29.4	1898	1 A45973	trichohyalin - hum
8	110	28.6	1407	1 S28589	trichohyalin - rab
9	106	27.6	613	2 S27770	hypothetical prote
10	105	27.3	1380	2 T14004	trifA protein - sil
11	105	27.3	1737	2 A59235	unconventional myo
12	100.5	26.2	385	2 T19201	hypothetical prote
13	99	25.8	523	2 T24961	hypothetical prote
14	99	25.8	1027	2 T46481	hypothetical prote
15	99	25.8	1233	2 T30989	serine/threonine p
16	98	25.5	648	1 J01150	protein kinase (EC
17	96.5	25.1	385	2 T20410	hypothetical prote
18	96	25.0	233	2 T17218	hypothetical prote
19	96	25.0	429	2 S29565	apolipoprotein A-I
20	96	25.0	524	2 J01730	62k sucrose-bindin
21	95.5	24.9	538	2 S29521	casein kinase I ho
22	95	24.7	849	2 S61962	probable membrane
23	94.5	24.6	678	2 A54514	glutamic acid-rich
24	94.5	24.6	839	2 I50590	class I INCENP pro
25	94.5	24.6	877	2 I50591	class II INCENP pr
26	94.5	24.6	1505	2 J54851	hypoxia-inducible
27	94	24.5	772	2 I50463	protein kinase - c
28	94	24.5	1023	2 S12519	glutactin - fruit
29	94	24.5	1085	2 S62516	hypothetical coile

30	94	24.5	1549	1 A40691	trichohyalin - she
31	93	24.2	1403	2 S24548	homoeotic protein p
32	92.5	24.1	758	2 S54522	hypothetical prote
33	92	24.0	139	2 A26892	Mopa box protein -
34	92	24.0	1057	2 H83273	ribonuclease E PA2
35	91	23.7	582	2 B53234	vicilin-like stora
36	91	23.7	766	2 H54024	protein kinase (EC
37	91	23.7	768	2 H54024	protein kinase (EC
38	91	23.7	777	2 F54024	protein kinase (EC
39	91	23.7	779	2 E54024	protein kinase (EC
40	91	23.7	783	2 A55817	cyclin-dependent k
41	91	23.7	905	1 R6BY55	regulatory protein
42	90.5	23.6	407	2 T02258	globulin1 - maize
43	90.5	23.6	540	2 S21825	vicilin-like stora
44	90.5	23.6	550	2 A46419	trophoblast-endoth
45	90.5	23.6	573	2 A53234	globulin-15, GLB15

ALIGNMENTS

RESULT 1
S22477
vicilin precursor - cacao
C:Species: Theobroma cacao (cacao)
C:Date: 30-Sep-1993 #sequence-revision 30-Sep-1993 #text-change 17-Mar-1999
C:Accession: S22477; S22478; S18105; S22050
R:McHenry, L., Fritz, P.J.
Plant Mol. Biol. 18, 1173-1176, 1992
A>Title: Comparison of the structure and nucleotide sequence of vicilin genes of coco
A:Reference number: S22477; MUID:92288309
A:Accession: S22477
A:Molecule type: DNA
A:Residues: 1-566 <MC2>
A:Cross-references: EMBL:X62625
A:Accession: S22478
A:Molecule type: mRNA
A:Residues: 1-452 <MC2>
A:Cross-references: EMBL:X62626
C:Genetics:
A:Introns: 211/1; 269/3; 296/3; 391/3; 502/1
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-566/Product: vicilin #status predicted <MAT>

Query Match 45.6%; Score 175; DB 2; Length 566;

Best local Similarity 32.4%; Pred. No. 1.4e-07;

Matches 33; Conservative 19; Mismatches 14; Indels 36; Gaps 2;

QY 3 QRRPQOQYECOCRCRQHETPRHNMOTCCORCERREKEREKKQ-----46

Db 35 ERPRQOYECOCRCSEATERRQECRCERKEKEDQREBELRLQYQOCGRQCE 94

OY 47 -----KRYEEOOREDEKEY-----EERMKED 68

Db 95 QQOQGRQOQOQCRKQWQYKREDERGHEHNTHNKMRSEEE 136

RESULT 2

FMCNAB
alpha-globulin B precursor (clone C72) - upland cotton

N:Alternate names: seed storage protein; vicilin precursor

C:Species: Gossypium hirsutum (upland cotton)

C:Date: 30-Sep-1991 #sequence-revision 30-Sep-1991 #text-change 16-Jul-1999

R:Accession: A30838; S06911

R:Chikan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.

Plant Mol. Biol. 7, 475-489, 1986

A>Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII

A:Reference number: A30838

A:Accession: A30838

A:Molecule type: mRNA

